

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 9, 2003, 16:24:23 ; Search time 15.5429 Seconds
(without alignments)
98.997 Million cell updates/sec

Perfect score: 16

Sequence: 1 CRRAAAARRARAAEA 16

Scoring table: OLIGO
Gapop 60.0 , Gapart 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_76.0

1: Piri;*
2: Pir2;*
3: pir3;*
4: Piri;*

Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	56.2	105	2 D86976	probable integrase
2	9	56.2	190	2 B70899	Probable mIFP Prot
3	8	50.0	336	2 T50935	'isomerase/decarbox
4	8	50.0	356	2 A11198	H-2 class I histoc
5	8	50.0	383	2 F83490	Probable multidrug
6	8	50.0	710	2 AD3479	ATP-dependent heli
7	8	50.0	897	2 T02808	conserved hypothet
8	8	50.0	998	2 T35745	Probable ATP-bindi
9	7	43.8	69	2 AD2110	hypothetical prote
10	7	43.8	77	2 AH0925	hypothetical prote
11	7	43.8	110	2 T30752	hypothetical prote
12	7	43.8	157	2 D70777	hypothetical prote
13	7	43.8	159	2 C83305	hypothetical prote
14	7	43.8	174	2 D87638	transcription regu
15	7	43.8	252	2 AH3618	high-affinity bran
16	7	43.8	263	1 C39741	hypothetical 29k P
17	7	43.8	292	2 JE0233	troponin-T - scal
18	7	43.8	336	2 E84295	hypothetical prote
19	7	43.8	358	2 F87364	HIYD family secret
20	7	43.8	376	2 T35868	Probable dipeptida
21	7	43.8	408	2 A87649	hypothetical Prote
22	7	43.8	409	1 S72892	probable hexosyltr
23	7	43.8	411	2 H82998	probable 3-hydroxy
24	7	43.8	428	2 H87214	probable glycosyl
25	7	43.8	438	2 T36953	conserved hypothet
26	7	43.8	444	2 S35733	glycoprotein gX -
27	7	43.8	474	1 BYBRC	Cya Protein - Bor
28	7	43.8	480	1 A70744	probable hexosyltr
29	7	43.8	501	2 A87474	enoyl-CoA hydrat

hypothetical prote
hypothetical prote
DNA repair protein
HNLFS5 protein - hu
forked protein - f
hypothetical prote
80.7K alpha trans-
hypothetical prote
hypothetical prote
glycoprotein gII P
membrane antigen P
zinc finger protein
IGA-specific serin
hypothetical prote
hypothetical prote
DNA-directed RNA P

ALIGNMENTS

RESULT 1

D86976

probable integration host factor [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001
C;Accession: D86976
R;Cole, S.T.; Eigenthaler, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.F.
R.; Davis, R.M.; Devlin, K.; Dutchoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Hoj
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, J;
A;Title: Massive gene decay in the leprosy bacillus
A;Reference number: A869309; PMID:21128732; PMID:11234002
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-105 <STO>
A;Cross-references: GB:AL450380; PMID:g13092744; PMID:GAC30048.1; GSPDB:GN00147
C;Genetics:
A;Gene: miHF

Query Match 56.2%; Score 9; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AAARRAAE 15
| | | | | | | | | |
Db 19 AAARRAAE 27

RESULT 2

Probable miHF protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998

C;Accession: B70899

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gor
Connor, D.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroy
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whithead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete ge
A;Reference number: A70500; PMID:9295387; PMID:9634230
A;Accession: B70899

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
A;Residues: 1-190 <COL>
A;Cross-references: GB:Z80108; PMID:GA123456; PMID:93256012; PMID:GAB02193.1; PID:9154
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: miHF
C;Superfamily: Mycobacterium tuberculosis probable miHF protein

A; Map position: 1
 Query Match 50.0%; Score 8; DB 2; Length 897;
 Best Local Similarity 100.0%; Pred. No. 13; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 Qy 7 AAARRARA 14
 Db 326 AAARRARA 333
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-77 <PAR>
 A; Cross-references: GB:AL513382; PIDN:CAD09426.1; PMID:916504543; GSPDB:GN00176

RESULT 8
 T33745 probable Arp-binding RNA helicase - Streptomyces coelicolor
 C;Species: Streptomyces coelicolor
 C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Nov-1999
 R; Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.
 submitted to the EMBL Data Library, August 1999
 A; Reference number: Z21588
 A; Accession: T33745
 A; Status: preliminary; translated from GB/EMBL/DDJB
 A; Molecule type: DNA
 A; Residues: 1-998 <SAU>
 A; Cross-references: EMBL:AL109732; PIDN:CAB52056.1; GSPDB:GN000070; SCOEDB:SC7H2.14
 A; Experimental source: strain A3(2)
 C;Genetics:
 A;Gene: SCOEDB:SC7H2.14

Query Match 50.0%; Score 8; DB 2; Length 998;
 Best Local Similarity 100.0%; Pred. No. 14; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 Qy 4 AAARRARR 11
 Db 70 AAARRARR 77

RESULT 9
 AD2110 hypothetical protein as12435 [imported] - Nostoc sp. (strain PCC 7120)
 C;Species: Nostoc sp. PCC 7120
 A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C;Accession: AD2110
 R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchiyama, N.; Shimpoo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001.
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena sp. number AB1807; PMID:21595205; MUID:11759840
 A; Accession: AD2110
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-69 <KUR>
 A; Cross-references: GB:BA000019; PIDN:BAB74134.1; PMID:917131527; GSPDB:GN00179
 A; Experimental source: strain PCC 7120
 C;Genetics:
 A;Gene: as12435

Query Match 43.8%; Score 7; DB 2; Length 69;
 Best Local Similarity 100.0%; Pred. No. 12; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0;
 Qy 7 AAARRAR 13
 Db 54 AAARRAR 60

RESULT 10
 AH925 hypothetical protein STR3665 [imported] - Salmonella enterica subsp. enterica serovar Typhi
 C;Species: Salmonella enterica subsp. enterica serovar Typhi
 A;Note: this species has also been called Salmonella typhi

C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C; Accession: AH925
 R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farman, S.; Moule, S.; O'Georain, P.
 Nature 413, 848-852, 2001.
 A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A; Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* ssp. *enterica*; Reference number: AB05022; MUID:2154947; PMID:11677608
 A; Accession: AH0225
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-77 <PAR>
 A; Cross-references: GB:AL513382; PIDN:CAD09426.1; PMID:916504543; GSPDB:GN00176
 A;Gene: STR3665

Query Match 43.8%; Score 7; DB 2; Length 77;
 Best Local Similarity 100.0%; Pred. No. 13; Gaps 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RRRAAEE 16
 Db 30 RRRAAEE 36

RESULT 11
 T30752 hypothetical protein 150R - *Molluscum contagiosum* virus 1
 N;Alternate names: MC150R
 C;Species: *Molluscum contagiosum* virus 1
 C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
 C;Accession: T30752
 R; Sankevich, T.G.; Bugert, J.J.; Sisler, J.R.; Roosin, E.V.; Darai, G.; Moss, B.
 Science 273, 813-816, 1996
 A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host genes
 A; Reference number: Z20876; PMID:9632549; PMID:8670425
 A; Accession: T30752
 A; Status: preliminary; translated from GB/EMBL/DDJB
 A; Molecule type: DNA
 A; Residues: 1-110 <SEN>
 A; Cross-references: EMBL:U60315; NID:gi491943; PIDN:AAC55278.1; PMID:gi492093
 C;Genetics:
 A;Note: MC150R
 C;Superfamily: *Molluscum contagiosum* virus 1 hypothetical protein 150R
 Query Match 43.8%; Score 7; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 17; Gaps 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AAARRAR 13
 Db 91 AAARRAR 97

RESULT 12
 D70777 hypothetical protein Rv2242 - *Mycobacterium tuberculosis* (strain H37RV)
 C;Species: *Mycobacterium tuberculosis*
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C;Accession: D70777
 R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyde, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, R.; Shelton, S.; Squares, S.; Whitehead, S.; Barrell, B.G.; A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.; A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A; Reference number: A70500; MUID:98295987; PMID:9634230
 A; Accession: D70777
 A; Status: preliminary; nucleic acid sequence not shown
 A; Molecule type: DNA
 A; Residues: 1-157 <COL>
 A; Cross-references: GB:Z70692; PIDN:CAA94666.1; PMID:e129

Sat Aug 9 19:18:31 2003

RESULT 3
 T5935 Query Match score .9; DB 2; Length 190;
 Best Local Similarity 100.0%; Pred. No. 0.56; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;
 Qy 7 AAARRAAE 15
 Db 104 AAARRARAE 112

C:Species: Pseudomonas abietaniphila
 C:Accession: F50935
 R:Martin, V.J.; Mohn, W.W.
 J: Bacteriol. 181, 2675-2682, 1999
 A:Title: A novel aromatic-ring-hydroxylating dioxygenase from the diterpenoid-degrading
 A:Reference number: Z25281; MUID:98235742; PMID:10217753
 A:Accession: T50935
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-336 <MARD>
 A:Cross-references: EMBL:AF119621; PIDN:ADD21070.1
 A:Experimental source: strain BRME-3; ATCC700689
 C:Genetics:
 A:Gene: dith

Query Match score 8; DB 2; Length 336;
 Best Local Similarity 100.0%; Pred. No. 5.9; 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;

Qy 7 AAARRAAE 14
 Db 105 AAARRARA 112

RESULT 4
 A21198 H-2 class I histocompatibility antigen PH-2D-24 - mouse
 C:Species: Mus musculus (house mouse)
 C:Accession: A21198
 R:Lalanne, J.L.; Cochet, M.; Kummer, A.M.; Gachelin, G.; Kourilsky, P.
 A:Note: the authors translated the codon CCC for residue 288 as Ser
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology <IM>
 F:205-270/Domain: immunoglobulin homology <IM>

Query Match score 8; DB 2; Length 356;
 Best Local Similarity 100.0%; Pred. No. 6.2; 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;

Qy 3 RAFAAAR 10
 Db 20 RAARRAAR 27

RESULT 5
 F83490 Query Match score .9; DB 2; Length 190;
 Best Local Similarity 100.0%; Pred. No. 0.56; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;
 Qy 1 AAARRAAE 15
 Db 104 AAARRARAE 112

C:Species: Pseudomonas aeruginosa
 C:Accession: F83490
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-960, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa
 A:Reference number: A82950; MUID:2043737; PMID:10984043
 A:Accession: PA1237
 A:Molecule type: DNA
 A:Residues: 1-383 <STO>
 A:Cross-references: GB:AE004553; PIDN:AAG04626.1; GSPDB:GN
 A:Experimental source: strain PAO1
 C:Genetics:
 A:Gene: PA1237 multidrug resistance protein A; lipoyl/biotin-binding homology
 C:Superfamily: multidrug resistance protein A; lipoyl/biotin-binding homology
 C:Species: Brucella melitensis (strain 16M)
 C:Accession: AD3479
 R:Alvechi, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
 i; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
 A:Accession number: AD3479
 A:Accession: AD3479
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-710 <KUR>
 A:Cross-references: GB:AE008917; PIDN:AAI52999.1; PID:917983853; GSPDB:GN00190
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMET11818
 A:Map position: I
 C:Superfamily: HrpB type ATP-dependent RNA helicase

Query Match score 8; DB 2; Length 710;
 Best Local Similarity 100.0%; Pred. No. 11; 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;

Qy 4 AAARRAARR 11
 Db 156 AAARRAARR 163

RESULT 7
 T02808 Query Match score .9; DB 2; Length 199
 Best Local Similarity 100.0%; Pred. No. 11; 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;

Qy 4 AAARRAARR 11
 Db 156 AAARRAARR 163

RESULT 7
 T02808 conserved hypothetical protein YPL199C, L2602.6 [imported] - Leishmania major (strai
 C:Species: Leishmania major
 C:Accession: T02808
 C:Map position: I
 C:Superfamily: conserved hypothetical protein YPL199C, L2602.6 [imported] - Leishmania major (strai
 C:Date: 24-Mar-1999 *sequence_revision 24-Mar-1999 *text_change 19-May-2000
 C:Accession: DB1457; T02808
 R:Myler, P.J.; Audleman, L.; devos, T.; Hixson, G.; Kissel, P.; Lemley, C.; Magness,
 Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
 A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of prot
 A:Reference number: AB1455; MUID:99178987; PMID:10077609
 A:Accession: D81457
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-89 <PYL>
 A:Cross-references: GB:AB001274; PIDN:AC24631.1; PID:92995584; GSPDB
 C:Genetics:
 A:Gene: L2602.6

A; Experimental source: strain H37Rv
 C; Genetics:
 A; Gene: Rv2322

Query Match 43.8%; Score 7; DB 2; Length 157;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 RAAARRA 12
 Db 66 RAAARRA 72

RESULT 13

CB3305 hypothetical protein PA2721 [Imported] - *Pseudomonas aeruginosa* (strain PA01)
 C; Species: *Pseudomonas aeruginosa*
 C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C; Accession: CB3305
 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, N.; Lozy, S.; Olson, M.V.
Nature 406, 959-964, 2000
 A; Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 A; Reference number: A82950; NID:20437337; PMID:10984043
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-159 <STO>
 A; Cross-references: GB:AE004700; GB:AE004091; NID:99948792; PIDN:AAGG06109.1; GSPDB:GN001
 A; Experimental source: strain PA01
 C; Genetics:
 A; Gene: PA2721

Query Match 43.8%; Score 7; DB 2; Length 159;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 RAAARRA 12
 Db 132 RAAARRA 138

RESULT 14

D87638 transcription regulator, GntR family [Imported] - *Caulobacter crescentus*
 C; Species: *Caulobacter crescentus*
 C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C; Accession: D87638
 R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonay, F.J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, R.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A; Title: Complete Genome Sequence of *Caulobacter crescentus*.
 A; Reference number: A87249; NID:21173638; PMID:11259647
 A; Accession: D87638
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-174 <STO>
 A; Cross-references: GB:AE005673; NID:913424808; PIDN:AAK25104.1; GSPDB:GN00148
 C; Genetics:
 A; Gene: CC1142

Query Match 43.8%; Score 7; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 AARAAR 10
 Db 50 ARAARR 56

RESULT 15

AH3618 high-affinity branched-chain amino acid transport ATP-binding protein livP BMEII08;
 C; Species: *Brucella melitensis*
 C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 17-May-2002
 C; Accession: AH3618
 R; DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivarsson, M.; Goitsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Iyer, R.; Mazur, M.; Goitsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Iyer, R.; Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A; Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
 A; Reference number: AD3232; PMID:11756688
 A; Accession: AH3618
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-252 <RUR>
 A; Cross-references: GB:AF008918; PIDN:AA54115.1; PID:917985076; GSPDB:GN00191
 A; Experimental source: strain 16M
 C; Genetics:
 A; Gene: BMEII0873
 A; Map position: II
 C; Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homologs
 Query Match 43.8%; Score 7; DB 2; Length 252;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 RAAARRA 8
 Db 121 RRAARRA 127

Search completed: August 9, 2003, 16:34:12
 Job time : 15:54:29 secs